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(54) **METHOD FOR GENE AMPLIFICATION**

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(30) **Foreign Application Priority Data**

Nov. 24, 2005 (JP) 2005-338119

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C12P 19/34 (2006.01)
C12Q 1/68 (2006.01)

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CPC ***C12P 19/34*** (2013.01); ***C12Q 1/6844*** (2013.01); ***C12Q 1/6867*** (2013.01)

(58) **Field of Classification Search**
None
See application file for complete search history.

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(57) **ABSTRACT**

The present invention provides a double-stranded DNA constructed specifically for high speed gene amplification, a method for gene amplification and a method for synthesizing protein. The gene amplification system of the present invention used a site-specific recombinase such as Cre-lox system and target sequence thereof to efficiently induce a type of replication referred to as a double rolling-circle replication (DRCR). Amplification unit, whose structure is shown in FIG. 2 (*a*), is constructed in animal and other cells. DRCR is induced by two recombination events triggered by a site-specific recombinase (Cre) when each replication folk progresses between each pair of target sequences (lox sequences).

15 Claims, 7 Drawing Sheets

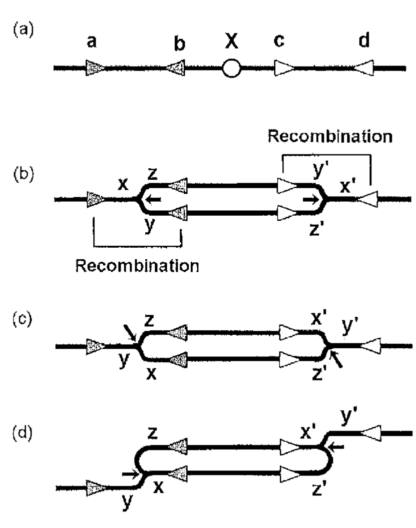

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Figure 1

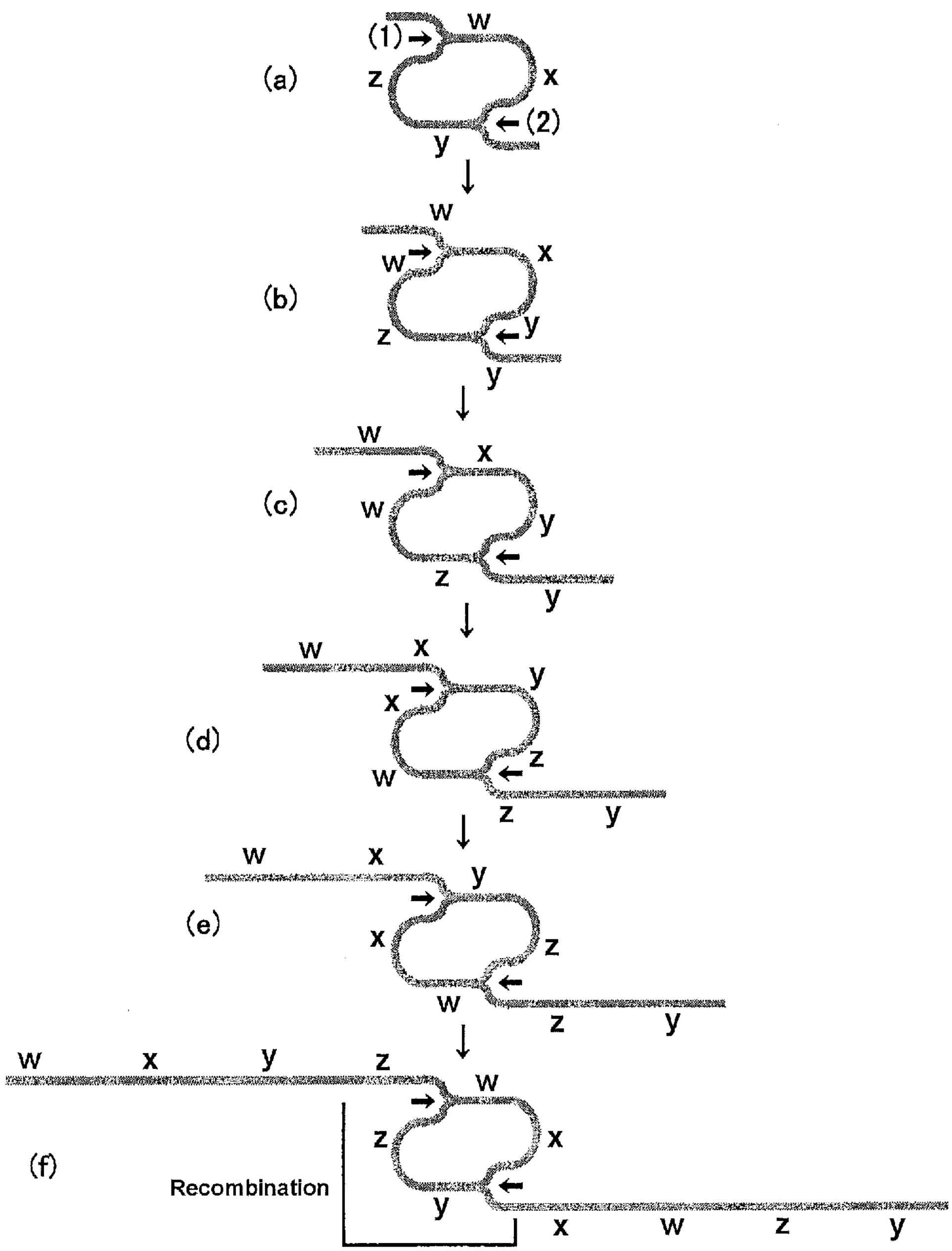


Figure 2

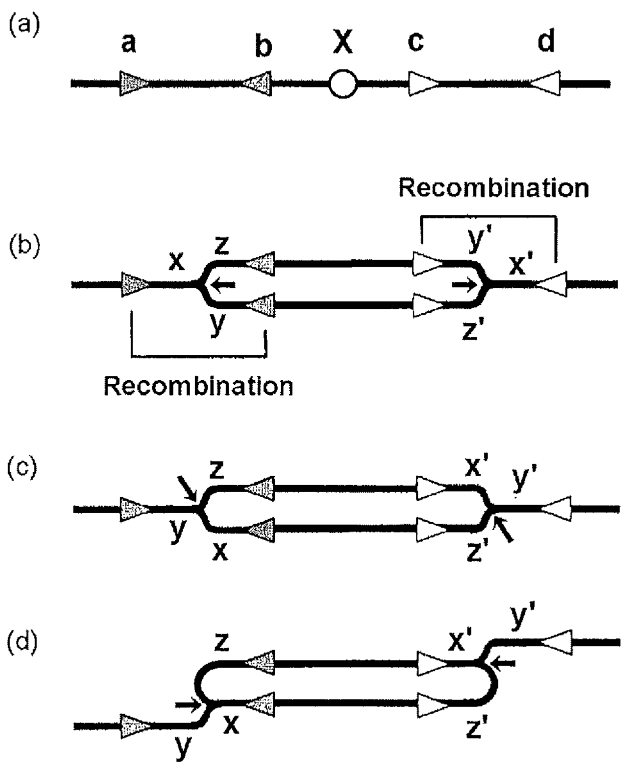


Figure 3

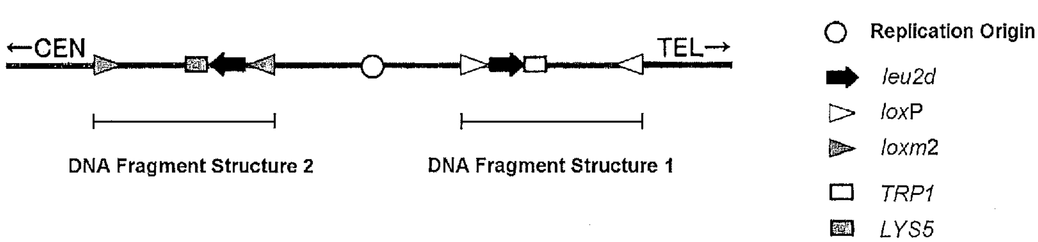


Figure 4

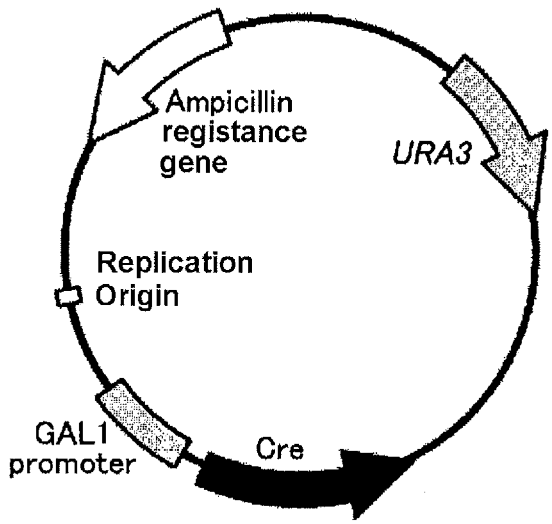


Figure 5

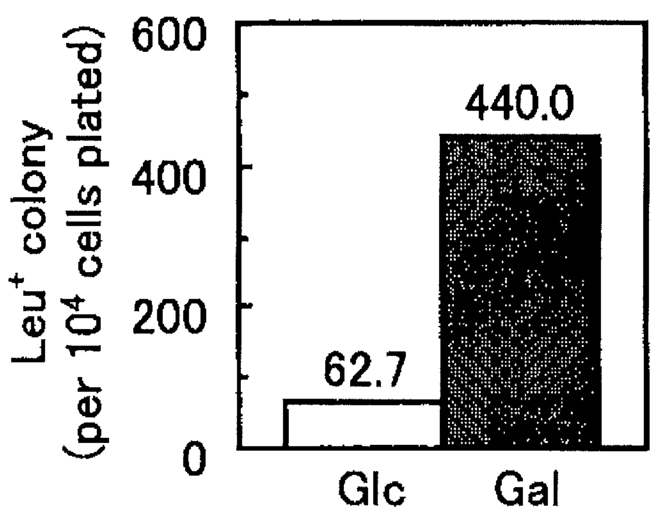


Figure 6

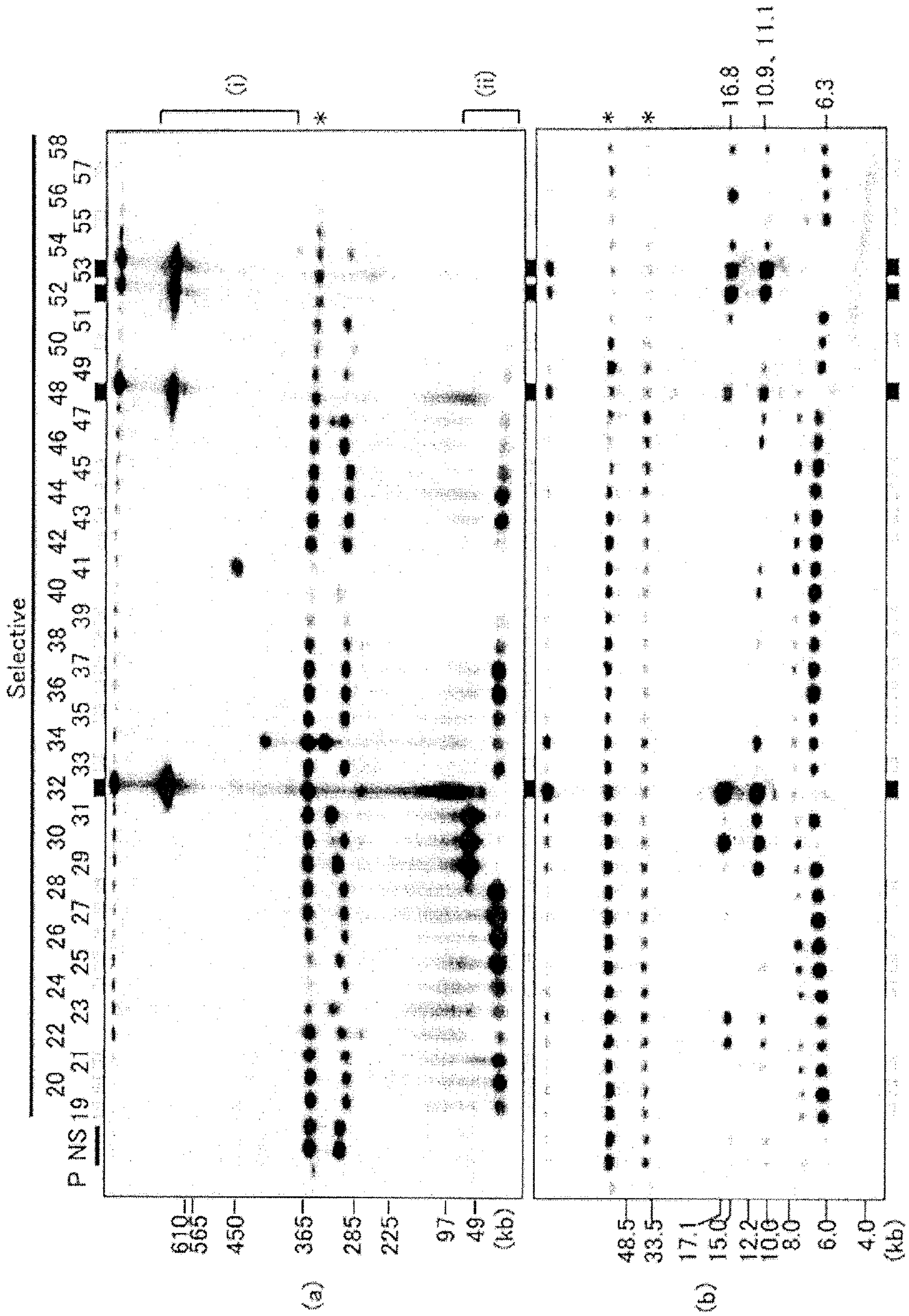

P NS 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58
Selective
(i)
(ii)
*
(a)
610
565
450
365
285
225
97
49
(kb)
(b)
48.5
33.5
17.1
15.0
12.2
10.0
8.0
6.0
4.0
(kb)
16.8
10.9, 11.1
6.3

Figure 7

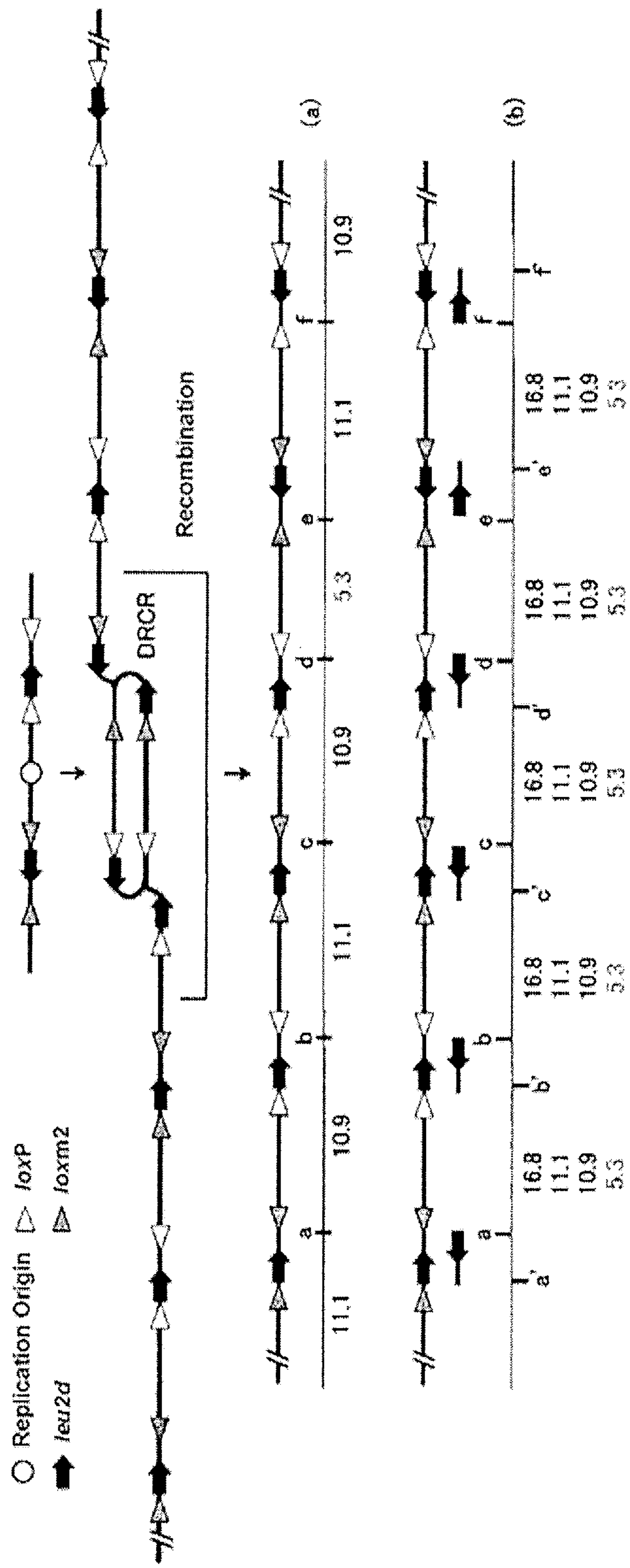

Replication Origin
loxP
leu2d
loxm2
DRCR
Recombination
(a)
a
b
c
d
e
f
11.1
10.9
11.1
10.9
5.3
11.1
10.9
(b)
a'
a
b'
b
c'
c
d'
d
e
e'
f'
f
16.8
11.1
10.9
5.3

Figure 8

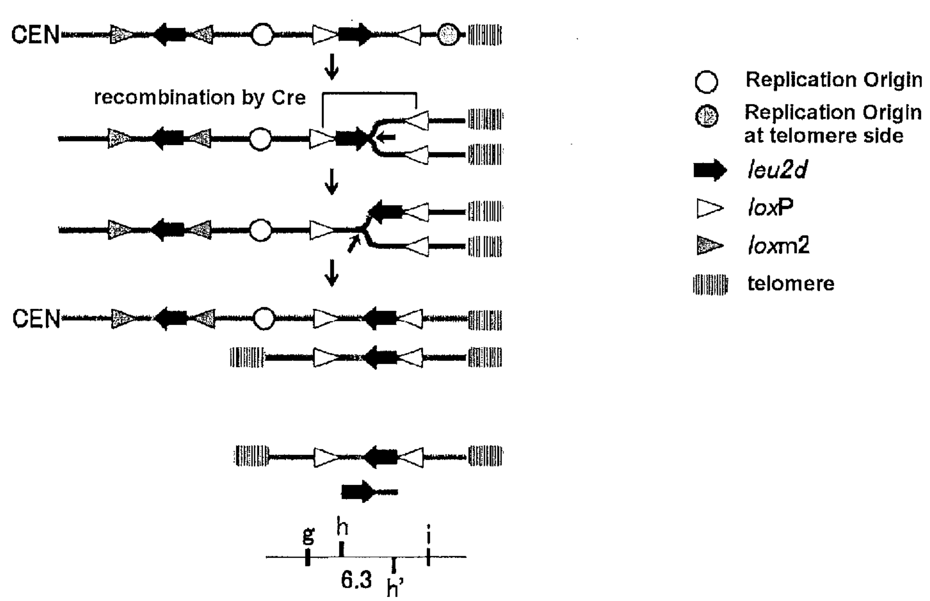


Figure 9

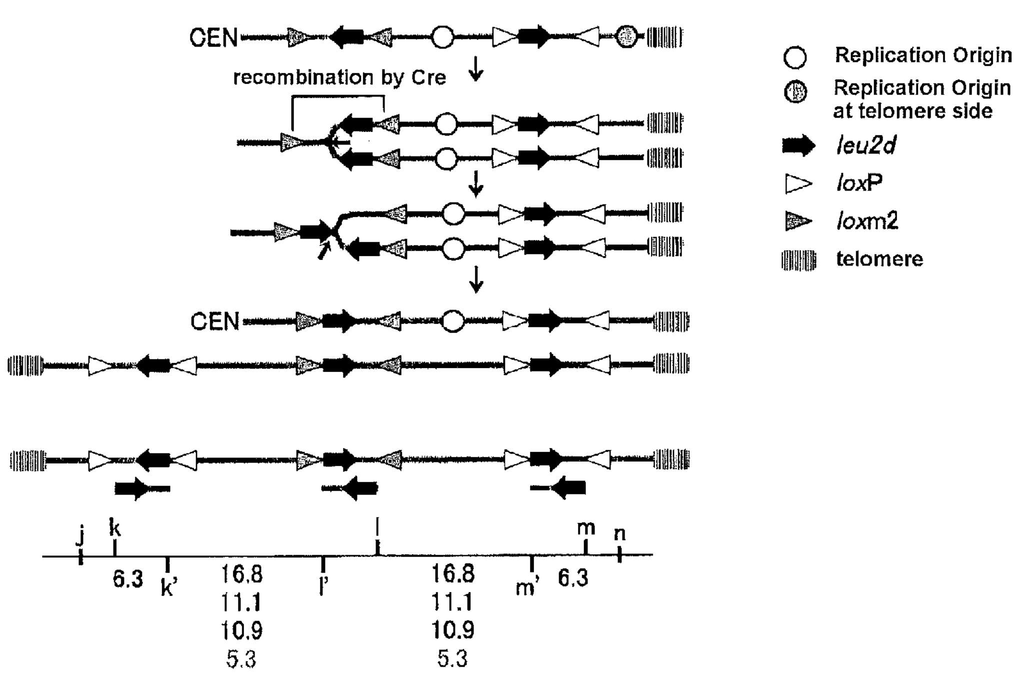
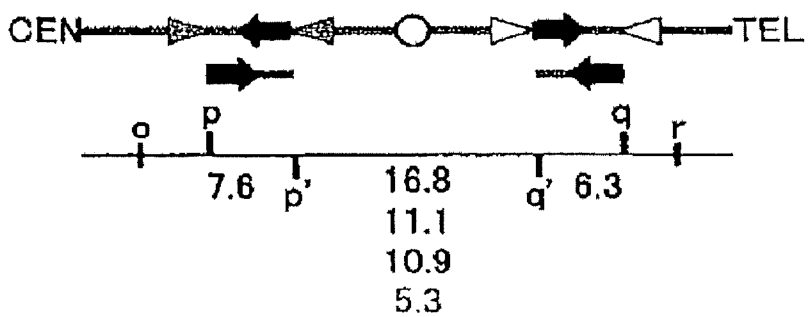


Figure 10



METHOD FOR GENE AMPLIFICATION

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. patent application Ser. No. 12/085,476, filed on May 23, 2008, which is a national stage application of International Application No. PCT/JP2006/314168, filed on Jul. 18, 2006, and which claims benefit of Japanese Patent Application No. 2005-338119 filed Nov. 24, 2005, the disclosures of each of which are incorporated herein in their entireties.

CROSS-REFERENCE TO RELATED DOCUMENTS

This application comprises a sequence listing filed in electronic form as an ASCII .txt file entitled 1680-26-2ST25.txt, created May 9, 2013, 2200 bytes (22 kilobytes). The content of the sequence listing is incorporated herein in its entirety.

FIELD OF THE INVENTION

The present invention relates to a method for amplifying gene at high speed and a method for producing proteins by using the amplified gene.

PRIOR ART

Gene amplification with cultured animal cells (Reference 1 and the like) accompanies several complications such as (1) time consuming (a half to one year), (2) presence of clones without amplification, and (3) empirical procedures with unexplained mechanism. On the other hand, there is no system of gene amplification with yeast. Although plasmids are generally used for the purpose, increase in copy number beyond a certain threshold is difficult.

The system of the present invention is based on the replication referred to as DRCR (Double Rolling-Circle Replication) induced by biological potency called as BIR (Break-Induced-Replication) (Reference 2-4). It is conceivable that a chromosome breakage is rescued itself by the following steps; i.e. the broken chromosome finds homologous sequence, invades into it, forms a replication fork, and consequently starts DNA replication. All living organisms might involve such ability.

Moreover, it is reported that natural circular DNA accompanies DRCR by recombination (Reference 5).

Reference 1: Japanese Patent Gazette 8-504585 (WO94/14968) Reference 2: WO2005/061703

Reference 3: PNAS, vol. 98, no. 15, 8255-8262 (Jul. 17, 2001)

Reference 4: Genes Dev 12, 3831-3842 (1998)

Reference 5: Cell. 1986 Aug. 15; 46 (4): 541-550

Problems to be Solved by the Invention

The present invention provides a double-stranded DNA constructed specially for high speed gene amplification, a method for gene amplification thereby and protein production thereby. The present invention is characteristic in full artificially designed system of gene amplification, the potential of higher amplification efficiency by synchronous culture, short period for amplification (probably one generation) and well elucidated mechanism of amplification.

Means to Solve the Problems

The amplification system of the present invention utilizes a type of DNA replication referred to as double rolling-circle replication (DRCR). The type of replication is able to amplify DNA explosively in a single cell cycle. It is assumed that the amplified products are maintained intracellularly after termination of DRCR by recombination and the like. The present inventors utilized a site-specific recombinase such as Cre-lox system and its target sequence in order to induce DRCR efficiently. More specifically, the present inventors constructed a replication unit (ex. FIG. **3**) in yeast and were able to succeed in inducing DRCR by utilizing a recombination generated by a site-specific Cre recombinase (hereinafter, referred to as "Cre") during progress of a replication fork between a pair of lox sequences and to accomplish the present invention.

Namely, the present invention is a double-stranded DNA represented by a-b-c-d or a-c-b-d, wherein one of a and b is a double-stranded DNA fragment comprising a first target sequence of a site-specific recombinase, and the other is a double-stranded DNA fragment comprising an inverted sequence of said first target sequence; and one of c and d is a double-stranded DNA fragment comprising a second target sequence of the site-specific recombinase and the other is a double-stranded DNA fragment comprising an inverted sequence of said second target sequence; a replication origin and at least one target gene to be amplified are inserted anywhere between a and d; and arbitrary DNA sequences may be inserted among above fragments.

Additionally, the present invention is a recombinant vector comprising the double-stranded DNA, and is also a transformant, which is introduced with the double-stranded DNA.

Moreover, the present invention is a set of double-stranded DNA comprising a double-stranded DNA fragment represented by e-a-A-b-f and a double-stranded DNA fragment represented by g-c-B-d-h, wherein one of a and b is a double-stranded DNA fragment comprising a first target sequence of a site-specific recombinase, and the other is a double-stranded DNA fragment comprising an inverted sequence of said first target sequence; and one of c and d is a double-stranded DNA fragment comprising a second target sequence of the site-specific recombinase and the other is a double-stranded DNA fragment comprising an inverted sequence of said second target sequence; each of letters from e to h is a double-stranded DNA fragment of at least 50 bp in size, which are arranged on a chromosome or an extrachromosomal element that is a host for integration of the set of double-stranded DNA in order of e, f, a replication origin of the chromosome element or the extrachromosomal element, g and h; at least one of A and B represents the target gene to be amplified; and said replication origin or a part of it may be included in f or g; and an arbitrary DNA sequence may be inserted among these.

The present invention is also a set of recombinant vectors, wherein each vector contains each of two kinds of the double-stranded DNA, and is also a transformant or transfectant, which is introduced with two kinds of the double-stranded DNA, wherein said replication origin locates on a host chromosome or an extrachromosome.

The present invention is also a method for amplifying the target gene, comprising the steps of preparing the transformant or the transfectant and affecting said transformants with the site-specific recombinase; and is a method for manufacturing a protein encoded by the target gene, comprising a step of culturing transformed or transfected cells obtained by the above method.

Effects of the Invention

The amplification system of the present invention has an excellent property in establishing efficient system for producing proteins. DRCR is capable of amplifying a target gene rapidly during a single cell cycle. Since the amplification mechanism is well elucidated, reliable amplification of a target gene is prospective. Although the present example was constructed in yeast not animal cells, it is possible to produce highly amplified products at 10 to 100 times higher frequency than a conventional system of animal cultured cells. Furthermore, the present system can be applied to primary cultured cells, in which gene amplification by drug selection has not been observed. Therefore, it is possible to apply gene amplification to targeting cells of gene therapy, and to enhance and sustain the expression of introduced gene.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** shows a DRCR reaction. Black arrowheads show replication folks.

FIG. **2** shows the initiation of the amplification reaction by using a site-specific recombinase and its target sequences. The triangular arrowheads (letters from a to d) represent the target sequences (e.g. loxP sequence) of a site-specific recombinase and the direction thereof. X represents replication origin (and so forth). Letters from x to z and x' to z' represent genes to be amplified. Black arrows represent replication folks.

FIG. **3** shows a construct for amplification. CEN: centromere, TEL: telomere.

FIG. **4** shows a plasmid (pSH47) for Cre expression.

FIG. **5** shows a colony forming frequency. Glc: glucose, Gal: galactose.

FIG. **6** shows the Southern blot analysis. (a) shows chromosomal DNA separated by PFGE and probed with leu2d, and (b) shows chromosomal DNA digested by SmaI and then separated by FIGE. Lane numbers from #19 to 58 show DNA prepared from colonies grown on the selective medium without leucine after Cre induction by galactose. NS shows DNA from control colonies grown on non-selective medium. P shows host cell lines. In this PFGE conditions, chromosomes with longer than about 650 kb are deemed to be concentrated above the separation limit.

FIG. **7** shows amplified products on chromosome. (a) shows the structure initially generated by DRCR. Letters from a to f represent the cleavage sites by restriction enzyme SmaI and digits show fragment size (kb). Nevertheless, 5.3 kb fragments generated by d-e cleavage are not detected by the Southern blotting, since the fragments do not include leu2d. (b) shows the structure with inversion (rearrangement to reverse direction) of the sequence between lox. Letters from a' to f' represent cleavage sites changed by inversion, and digits show predicted fragment size (kb). For example, a-b cleavage produces 10.9 kb fragment. In a case of inversion of the region containing a, a'-b cleavage produces 16.8 kb fragments. Similarly, a-b' cleavage produces 5.3 kb fragment and a'-b' cleavage produces 11.1 kb fragment. The 5.3 kb fragment, which does not contain leu2d gene, is undetectable by the Southern blotting.

FIG. **8** shows amplified products on a mini chromosome (FIG. **6** (ii)). Replication from the telomere side proceeds to reverse direction due to recombination between loxP, and produces mini chromosome (about 18 kb in size) with telomere at the both ends. The SmaI cleavage sites from g to i and site h' changed by inversion produce 6.3 kb fragments containing leu2d (The fragment is derived from g-h' or h-i fragment. The fragment g-i cannot be generated because of cleavage at either h or h' site).

FIG. **9** shows amplification products on a mini chromosome (FIG. **6** (ii)). Replication from the telomere side proceeds to reverse direction due to recombination between loxm2 and produces a mini chromosome (about 40 kb in size). Letters from j to n represent SmaI cleavage sites and letters from k' to m' represent cleavage sites changeable by inversion. Digits show possible fragment size (kb). The 5.3 kb fragment, which does not contain leu2d gene, is undetectable by the Southern blotting.

FIG. **10** shows the effect of Cre recombination on not amplified structure. The sequences between lox pairs can be frequently inverted. Letters from o to r represent SmaI cleavage sites, p' and q' represent the cleavage sites changeable by inversion and digits show possible fragment size (kb). The 5.3 kb fragment, which does not contain leu2d gene, is undetectable by the Southern blotting.

DETAILED DESCRIPTION OF THE INVENTION

The gene amplification method of the present invention utilizes a double rolling-circle replication (DRCR), which enables a rapid amplification, and is presumed to be functional both in budding yeasts and in animal cells. The gene amplification system is a type of DNA replication, wherein two replication folks replicate continuously a circular DNA, as shown in FIG. **1**. In the beginning, folk (1) replicates w and folk (2) replicates y ((a), (b), (c)), then folk (1) and folk (2) replicates x and folk (2) replicates z ((c), (d), (e)). In this way, the replication continues endlessly, since a template for one folk is synthesized by the other folk successively.

After the amplification has proceeded, the central circular form seems to be removed by recombination and the like, and the reaction seems to be terminated (f).

The gene amplification system of the present invention utilizes a site-specific recombination, which is known to be functional even in animal cells, in order to induce DRCR. This reaction is a reversal of DNA replication by recombination during progression of the replication folk between a set of target sequences. A pair of the reactions is used for the amplification system.

Namely, in the amplification system of the present invention, firstly, DNA replication starts in the amplification unit constructed as in FIG. **2** (*a*). Secondly, the two replication folks represented by black arrows go just between two sets of target sequences (lox sequences) of a site-specific recombinase (e.g. Cre). Lastly, the target sequences (e.g. loxP sequences) on parent DNA strand x and x' recombine with the target sequences (e.g. loxP sequences) on de novo DNA strand y and y', respectively. After the recombination events, one of the folks synthesizes y and z strands from x strand and the other folk synthesizes y' and z' strands from x' strand (FIG. **2** (*c*)). In this way, the progress of each replication folk is reversed and the replicated DNA strands are replicated again (FIG. **2** (*d*)). DRCR is carried out by these two reactions.

The double-stranded DNA used in the present invention is represented by a-b-c-d or a-c-b-d, or preferably by a-b-c-d.

One of a and b represents a double-stranded DNA fragment comprising a first target sequence of a site-specific recombinase, and the other represents a double-stranded

DNA fragment comprising inverted sequence of the first target sequence of the site-specific recombinase. One of c and d represents a double-stranded DNA fragment comprising a second target sequence of a site-specific recombinase, and the other represents a double-stranded DNA fragment comprising inverted sequence of the second target sequence of the site-specific recombinase. The first target sequence could be the same as the second target sequence, but is preferably different from the later. Additionally, arbitrary DNA sequence may be inserted between these sequences.

The above b and c may be combined and the DNA may be represented by a-b-d, wherein d and a represent the same target sequence with the same direction.

Moreover, the sequence may be represented by a-b-X-c-d or a-c-X-b-d, preferably by a-b-X-c-d, wherein X represents a replication origin. The replication origin includes Ori beta located at the 3' down stream of dihydrofolate reductase (DHFR) gene, latent origin (OriP) of EBV, origins located at the vicinity of c-myc gene or others, as a candidate, and may include any origin with replication initiation activity in animal cells.

Furthermore, the sequence may be represented by a-A-b-X-c-B-d or a-A-c-X-b-B-d, preferably by a-A-b-X-c-B-d, wherein at least one of A and B represents target gene. If a number of target genes are used, they can be the same as or different from each other. DRCR (FIG. **2**) explained above are similarly induced in these sequences.

A site-specific recombinase catalyzes the recombination between two short consensus DNA sequences (target sequences). The site-specific recombinase can induce site-specific recombination between the target sequences, change the target site further and modify the integrated gene.

The present invention may use the following site-specific recombinase and the target sequences specific to the recombinase (i.e. see; Developmental Cell, Vol. 6, 7-28, January 2004 and the like).

(1) Cre Recombinase or Derivatives Thereof.

Cre recombinase of bacterial virus P1 is applied most extensively to gene transfer and knockout in mouse. Cre protein catalyzes the recombination between two 34 base pair loxP recognition sites. The loxP sequence has a unique construction, wherein core 8 base pair sequence is flanked by two 13 base pair palindrome sequences. The asymmetric 8 base pair sequence determine the orientation of loxP site. DNA cleavage and recombination between loxP sites by Cre enzyme occur at a site between the rear of the first base and the front of the last base of the 8 base pair core sequence. Derivatives of the Cre enzyme are constructed by amino acid substitutions. The derivatives include site-specific recombinases, wherein wild type Cre recombinase is changed in its function and character by introduction of amino acid substitution; and site-specific recombinases and their genes, wherein mutations are introduced into wild type Cre recombinase gene to optimize CpG content, Kozak sequence related to translation initiation efficiency and codon-usage in host cells to increase expression efficiency and level. At least 29 kinds of Cre enzyme derivatives have been constructed. Derivatives thereof have different recombination activities and recognize different target sequences. Also, a number of mutated sequences are prepared for target sequence recognized by Cre enzyme. The present invention may use all above derivatives. Target sequences like above include loxP, lox511, lox5171, lox2272, lox2372, loxm2 (referred also as m2), loxFAS, lox71, lox 66 and mutants thereof. The mutant refers to a target sequence of site-specific recombination, wherein the sequence contains mutation introduced in one or more bases in wild type loxP sequence.

Although the recombination efficiency is generally sensitive to any change in lox sequences, mutants keeping function thereof were found. In the latter case, recombination may occur efficiently between pairs of homotypic loxP sites, but not between heterotypic sites.

(2) Flp Recombinase or Derivatives Thereof.

The recombinase is Flp recombinase derived from budding yeast. The activity of the recombinase is similar or slightly inferior to that of Cre/loxP. However, the activity of the recently developed active type Flp (Flpe) is improved and is similar to that of Cre. The consensus 34 base recombination sequence is referred to as FRT. Although the structure of FRT has the same structure as loxP, the sequence is different from each other.

Derivatives thereof refer to site-specific recombinases, wherein wild type Flp recombinase is changed in its function and character by introduction of amino acid substitution; and site-specific recombinases and their genes, wherein mutations are introduced into wild type Flp recombinase gene to optimize CpG content, Kozak sequence related to translation initiation efficiency and codon-usage in host cells to increase expression efficiency and level. At least 28 kinds of Flp enzyme derivatives have been constructed.

A number of derivatives have been constructed also for Flp enzyme and its recognition sequence. The target sequence includes FRT, F3, F5, FRT mutant−10, FRT mutant+10 and mutants thereof. The mutant refers to a target sequence of site-specific recombination reaction, wherein the sequence contains mutation introduced in one or more bases of wild type FRT sequence and the like.

Flp enzyme is very sensitive to the change in the sequence of FRT site, similar to Cre enzyme. Several mutant FRT pairs that lead to efficient recombination between homotypic sites are identified. However, recombination does not occur between different mutant FRT sites or between wild and mutant sites.

(3) PhiC31 Integrase or Derivatives Thereof.

PhiC31 integrase is derived from bacterial virus in Streptomyses and is functionable in human cells. The target sequence of the integrase includes attP, attB and their mutants. A mutant refers to a target sequence of the site-specific recombination, wherein the sequence contains mutation in one or more bases in wild type attP sequence and the like.

The enzyme induces recombination between a pair of three nucleotides, ttg, in the attPP' and attBB'. Since the sequences at both sides of 'ttg' are unique, the sequences are changed to different sequences from the original recognition sequences after recombination. Therefore, the enzyme cannot recognize the consequent sequence as a target site. Therefore, the recombination by the enzyme occurs only once.

The derivatives of PhiC31 integrase system refer to site-specific recombinases, wherein wild type PhiC31 integrase is changed in its function and character by introduction of amino acid substitution, and site-specific recombinases and their genes, wherein mutations are introduced into wild type PhiC31 integrase gene to optimize CpG content, Kozak sequence related to translation initiation yield and codon-usage in host cells to increase expression efficiency and level.

Cre/Lox system is preferable among the site-specific recombinase and target sequence thereof.

Furthermore, it is preferable that a target gene to be expressed, selective gene (drug resistant genes for Geneticin, Neomycin, Hygromycin, Zeocin, Blasticidin or the like) for selecting cells that contain the present construct in a chromosome or an extrachromosomal element, and a marker gene (dihydrofolate reductase (DHFR), glutamine synthetase (GS), aspartate transcarbamylase (CAD), metallothionein (MT), adenosine deaminase (ADA), adenylate deaminase (AMPD1,2), UMP synthetase, P-glycoprotein (P-gp), asparagine synthetase (AS), ornithine decarboxylase (ODC) or the like) for selecting cells with gene amplification may be inserted in arbitrary site within the structure. It is preferable to insert nuclear matrix attachment region (MAR) DNA, which is deemed to be important for amplification in animal cells. Additionally, arbitrary DNA sequence could be inserted between the above fragments.

The above fragments are appropriately connected by conventional method of genetic engineering.

The double-stranded DNA fragments thus obtained are transduced into appropriate cells by the methods of virus, lipofection, electroporation or the like. Furthermore, it is preferable to establish cell lines by selecting the cells that contain the above construct on a chromosome or an extrachromosomal element, by the drug corresponding a drug resistant gene (a drug resistant gene to Geneticin, Neomycin, Hygromycin, Zeocin, Blasticidin or the like). Yeast cells and animal cells can be used as the host. Pharmaceutical proteins are produced preferably in animal cells, wherein glycosylation pattern is similar to human and it reduces risk to undesirable immunological response. Animal cells include CHO (Chinese hamster ovary) cells used frequently for protein production as well as other cells derived from human, mouse, rat and other animals.

Furthermore, the double-stranded DNA of the present invention comprises one set of double-stranded DNA fragments obtained by dividing any of the above double-stranded DNA fragments into at least two, preferably 2 to 5, and more preferably two, wherein the DNA fragment comprises partial sequence of a host chromosome or an extrachromosomal element, and may contain at least 50 bp and preferably from 500 to 1 Kbp sequences at both ends for homologous recombination. The double-stranded DNA fragment for homologous recombination can produce the above double-stranded DNA on a host chromosome or an extrachromosomal element by homologous recombination.

The replication origin may be replication origin of the host chromosome or an extrachromosomal element; or an exogenous replication origin.

Moreover, the extrachromosomal element refers to replicable sequence in host cells derived from plasmid or virus, fragments of a host chromosome or an artificial chromosome.

A set of double-stranded DNA fragments thus described include the following examples:

(1) Double-stranded DNA referred to as e-a-A-b-f and double-stranded DNA referred to as g-c-B-d-h;

(2) Double-stranded DNA referred to as e-a-A-f and double-stranded DNA referred to as g-b-c-B-d-h;

(3) Double-stranded DNA referred to as e-a-f and double-stranded DNA referred to as g-A-b-c-B-d-h;

(4) Double-stranded DNA referred to as e-a-A-b-c-f and double-stranded DNA referred to as g-B-d-h;

(5) Double-stranded DNA referred to as e-a-A-b-c-B-f and double-stranded DNA referred to as g-d-h;

(6) Double-stranded DNA referred to as e-a-A-b-B-f and double-stranded DNA referred to as g-d-h;

(7) Double-stranded DNA referred to as e-a-A-f and double-stranded DNA referred to as g-B-d-h;

(8) Double-stranded DNA referred to as e-a-f and double-stranded DNA referred to as g-A-b-B-d-h.

In the above sets of double-stranded DNA, letters from a to d, A and B are similar to the above description. However, d in (6) to (8) refers to the same target sequence with the same orientation as "a".

Letters from e to h refer to the double-stranded DNA fragments comprising nucleotide sequences with size at least 50 bp, and preferably from 500 to 1 Kbp, wherein these DNA fragments are aligned in the order of e, f, replication origin, g, and h on a cellular chromosome or on an extrachromosomal element; and arbitrary sequence may be inserted between these fragments; and replication origin or a part of it may be included in f or g.

These fragments are connected as above.

At least two double-stranded DNA fragments thus obtained are introduced into appropriate cells by methods such as virus, lipofection, electroporation and the like. Furthermore, it is preferable to establish cell lines by selecting the cells that contain the above construct on a chromosome or an extrachromosomal element, by the drug corresponding a drug resistant gene (a drug resistant gene corresponding to Geneticin, Neomycin, Hygromycin, Zeocin, Blasticidin or the like). Yeast cells and animal cells can be used as the host. Pharmaceutical proteins are produced preferably in animal cells, wherein glycosylation pattern is similar to human and it reduces risk to undesirable immunological response.

Owing to the arrangement from e to h in the order and homologous recombination of these fragments with corresponding region in a host chromosome or an extrachromosomal element, similar construction to the above is generated on a host chromosome or on an extrachromosomal element.

The transformed or transfected cells thus obtained are subjected to the action of a site-specific recombinase. At the time of the action, it is preferable that site-specific recombinase works in the cells that are actively proliferating and progressing the cell cycle, or are synchronized in S phase, since enrichment of cells in replication phase (S phase) in cell cycle is preferable.

Methods for introducing the above site-specific recombinase include, for example, a method comprising the following steps:

(1) introducing a plasmid constructed to express said site-specific recombinase;

Various expression vectors are inserted with the site-specific recombinase gene under the control of promoter functional in a host cell. The vector is transfected into the above transformed or transfected cells by lipofection, electroporation method or the like. It is preferable to use inducible promoters to induce site-specific recombinase to actively proliferating cells.

(2) transforming the transformants or transfectants further to express said site-specific recombinase;

A construct, containing the site-specific recombinase gene under the control of promoter functional in a host cell and any of drug resistant genes against Geneticin, Neomycin, Hygromycin, Zeocin, Blasticidin or the like for selecting cells that contain the above construct on a chromosome or an extrachromosomal element, is prepared. The construct is introduced into the above transformed cells by lipofection, electroporation or the like. The construct containing the above DNA fragments is preferably linearized for efficient integration into a chromosome or to an extrachromosomal element. Additionally, inducible promoters are preferably used to induce site-specific recombinase to actively proliferating cells.

(3) introducing directly said site-specific recombinase protein.

Site-specific recombinase is prepared by expressing and purifying large amount of the enzyme. The enzyme is introduced into the above transformed cells using commercial protein delivery reagent (i.e. Targeting System Co., Profect; Genlantis Co., BioPORTER Protein Delivery Reagent) and the like. It is preferable to introduce the site-specific recombinase into cells actively proliferating and progressing the cell cycle, or into cells synchronized in S phase, since the site-specific recombinase should be induced into actively proliferating cells.

In the stage, wherein the site-specific recombinase acts, one of the replication folks must be located between two first target sequences and the other replication folk must be located between two second target sequences after initiation of the replication (FIG. **2** (*b*)). However, it is not necessary that all of the prepared cells are affected with the site-specific recombinase in such a specific situation. Since practically DNA replication in a number of cells is in various situations, it is enough for part of cells to be in such a specific situation. The target gene is amplified explosively in the cells in the above situation. Therefore, only a fraction of cells are good enough to be amplified.

Although amplification is induced as above description, it is preferable to select the cells with amplified DNA by drugs corresponding to target gene to be amplifieds (dihydrofolate reductase (DHFR), glutamine synthetase (GS), aspartate transcarbamylase (CAD), metallothionein (MT), adenosine deaminase (ADA), adenylate deaminase (AMPD1, 2), UMP synthetase, P-glycoprotein (P-gp), asp aragine synthetase (AS), ornithine decarboxylase (ODC) and the like). Those cell lines with high level of expression of a target gene are thus selected, and cultured. Large amount of the protein encorded by the target gene is prepared by purification from the culture medium or supernatant.

The following examples illustrate the present invention, but are not intended to limit the scope of the present invention.

Example 1

In this example, a construct (FIG. **3**) for amplification was composed.

Firstly, a DNA fragment structure 1 (structure of telomere side) was constructed, wherein the DNA fragment structure 1 contains a pair of loxP sequences with inverted arrangement, amplification-selection marker gene leu2d, and TRP1 gene, (SEQ ID NO.1, bases 1-34 of structure 1 is loxP sequence, bases 36-1988 is amplification marker gene leu2d, bases 1993-2845 (complementary strand) is TRP1 gene, and bases 5699-5732 is loxP sequence of inversion).

A DNA fragment was constructed, wherein the DNA fragment structure 1 is linked PCR fragment of bases 263177-264016 (SEQ ID No. 3) of chromosome 6 (Genebank Accession No. NC_001138) to the upstream of the DNA fragment structure 1 and linked PCR fragment of bases 264017-264685 (SEQ ID No. 4) of chromosome 6 (Genebank Accession No. NC_001138) to the downstream of the DNA fragment structure 1. Host yeast cells lines were transformed with the DNA fragment by Frozen-EZ Yeast Transformation II (ZYMO RESEARCH Co.). TRP1 marker gene allows cells to form colonies on agarose medium without tryptophan. The chromosomal structure of the selected cells was analyzed and cell lines with inserted structure flanked by loxP pair were established.

Then, DNA fragment structure 2 (structure of centromere side) was constructed, wherein the DNA fragment structure 2 contains a pair of loxm2 sequences with inverted arrangement, amplification-selection marker gene leu2d, and LYS5 gene, ((SEQ ID NO.2, bases 1-34 of structure 2 is loxm2 sequence, bases 3936-5888 (complementary strand) is amplification marker gene leu2d, bases 2891-3930 is LYS5 gene, and bases 5890-5923 is loxm2 sequence of inversion)).

A DNA fragment was constructed, wherein the DNA fragment structure 2 is linked PCR fragment of bases 257941-258821 (SEQ ID No. 5) to the upstream of the DNA fragment structure 2 and linked PCR fragment of bases 258822-259719 (SEQ ID No. 6) to the downstream of the DNA fragment structure 2. The DNA fragment was introduced into cells containing the above DNA structure 1 (a structure flanked by loxP pair). LYS5 marker gene allows cells to form colonies on agarose medium without lysine. The chromosomal structure of the selected cells was analyzed and cell lines with inserted structures flanked by loxP pair and loxm2 pair were established.

Additionally, amplification-selection marker gene leu2d lacks most of the promoter sequence and the expression level is very law. Therefore, the gene can complement leucine auxotrophy only when amplified.

It has been observed that Orc1 protein involved in replication initiation binds to the region between the above two DNA fragment structures (nature, 424: 1078, 2003). Therefore, the DNA region is supposed to be functional as replication origin. Furthermore, the DNA region contains WTTTAYRTTTWB (SEQ ID No.: 7), which is a consensus sequence of replication origin in Saccharomyces cerevisiae (bases 258889-258900).

Example 2

In this example, the construct (FIG. **3**) obtained in Example 1 was inserted to chromosome 6 of Saccharomyces cerevisiae, Cre gene was expressed and the double rolling-circle replication (DRCR) was induced.

The plasmid (FIG. **4**, Genebank Accession No. AF298782, gifted from University of Washington, Yeast Resource Center), wherein Cre gene (SEQ ID No.:8) is linked to the down stream of GAL promoter, was introduced into Saccharomyces cerevisiae cell line obtained in Example 1 by Frozen-EZ Yeast Transformation II (ZYMO RESEARCH). Furthermore, URA3 marker gene allows cells to form colonies on agarose medium without uracil.

The Ura^+ cells with the plasmids obtained above were cultured for three hours in liquid medium supplemented with galactose to induce Cre expression or glucose to suppress Cre expression as control. These cells were plated on glucose agar plate without leucine and then Leu^+ colonies were counted. The Leu^+ cells were further cultured and chromosomal DNA was prepared using low-melting temperature agarose.

The chromosomal DNA was separated by pulsed-field gel electrophoresis (PFGE, BIO-RAD, CHEF Mapper XA, Auto Algorithm, range: size from 220 to 500 kb), or the DNA digested with a restriction enzyme, SmaI, was separated by Field-inversion gel electrophoresis (FIEG, BIO-RAD, CHEF Mapper XA, Auto Algorism, range: size from 3 to 50 kb) and were analyzed by Southern blotting.

Result and Interpretation

The Leu^+ colony counts showed that there was about seven folds increase in colony forming activity in the case of induction of Cre expression in contrast to the control (addition of glucose) the induction of Cre expression gave about seven-fold higher frequency of Leu^+ colonies than the control condition as shown in FIG. **5**. The result strongly suggests that the Cre recombination contributes to the amplification.

Then, FIG. **6** (*a*) shows the result of structural analysis of chromosomal DNA, which is separated by PFGE, by Southern blotting using leu2d as a probe. As shown in FIG. **6**(*a*), amplified product (i) on chromosome 6, wherein the construct for amplification is inserted, and (ii) multi-copies of mini-chromosome were detected. Additionally, chromosome 3 (*) of host cell lines containing leu2 fragments at 345 kb in size, chromosome 6 containing the construct for amplification originally (e.g. NS) or containing slight amplification at size from 290 to 320 kb were detected.

Then, the above chromosomal DNA was digested with a restriction enzyme (SmaI) and separated by FIGE. The result of Southern blot for structural analysis using leu2d probe is shown in FIG. **6**(*b*).

Based on these results, the structure of the amplified product was elucidated as follows.

SmaI fragments with about 11 kb (10.9 and 11.1 kb) and 17 kb (16.8 kb) in size were detected from clones with strong signal highly amplified products (i) on chromosome (FIG. **6** (*a*) (i) #32, 48, 52, 53: black lanes). These fragments were derived from the product with inversions through lox pairs in a designed DRCR product and deemed to contain highly repeated sequence containing leu2d with at least more than several tens of copies, as shown in FIG. **7**.

In contrast, mini chromosome (FIG. **6** (ii)) observed in most of clones (grey lanes) generated SmaI amplified fragments at about 6.3 kb in size. It is interpreted that these fragments are generated through reversal of replication from telomere side of the structure by Cre-loxP recombination, and that these fragments present as multi-copies, as shown in FIG. **8**.

In addition to the above fragments, chromosomal products without inversions (FIG. **7**(*a*), #34, 41, 47) and other types of mini chromosome (FIG. **9**, #29-31, 49, 56) through reversal of replication by similar recombination are observed. Furthermore, a number of clones containing both amplified product on chromosome and mini chromosome are detected (#22, 31, 34, 41, 47, 58). Also, weak signal originating from four fragments in addition to two SmaI fragments (* of FIG. **6** (*b*)) derived from host cell lines are confirmed in the construct not amplified (NS of FIG. **6** (*b*), FIG. **10**).

Highly amplified products through the expected molecular mechanism was observed (#32, 48, 52 and 53). Since these products are observed in one tenth of the analyzed clones, these type of amplification occurred at frequency of one tenth of the total colony forming frequency 4.4%, i.e. 0.44%.

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atattacact gccgccgcct tccatgcctt tggaaagcag acaatgatgc taggcggcgc    180

ccagcagtat aaacttttct tgcttataac cagaacctct atcacaaaat tagaaactgc    240

gatactatgg gtcagatcga cacataggga gcactattag gcgcaaggcg tatacatagg    300

cattgcgtgt tcaaaaattg tcgtatgaga aaagttccaa actttccacc attactcacc    360

aacaacttac accagcccgg atttaagatt tagcttccga gaatattgtg actcagccac    420

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gttctgaaat ttttaaagtt tagcacacca tattcacgct cgaggtgaac ccaagttttc    600

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gccaagttcg gtgttgaaac ggattattat gacccatcaa tagggaagga tatagaaaaa 600

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<213> ORGANISM: Saccharomyces cerevisiae

<400> SEQUENCE: 5

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acggactgat gcacttttcc attgtacgat aacattactt acaagattgg gagaagcatg 240

attgaaaatt tgactggaag aaccacttat attaggagtg gcggtattag tagaaaattg 300

actaaacgca tccgaaaatt aaatagaatt taaagtttcc ttgggtgcac tgttttgggc 360

tgcagtgcta aaatccagaa gtgttggagt caggttactt gtttgcatac agacattact 420

gaagttttca gaaggccttt gaatcgagaa cgagataagg aagtgtcctc taaatgcaat 480

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gatgaaacag aaaatatgta ttttatggat tgactaatca agtcacttgc tgattgtgta 780

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<212> TYPE: DNA
<213> ORGANISM: Saccharomyces cerevisiae

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aatctggaag atgcattcgt cgattggcct tcattaagtg aagattggta acctattgca    180

tccaaaccag aagtaataca accagaatgt ggagatgagg agccaacagg tgtgtatcca    240

gaaggttcag ccacaggttg gtcatcaata ccactggggg agcatgcaat ataatcagat    300

ggttgcgagg aatagctagt agagctaaaa ctgaacacat tagttaagat tagactagcc    360

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gatttttaga ttattatcat ggaaccaagt tgatgtcttg caatttctga tttttaacga    840

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<222> LOCATION: (1)..(12)
<223> OTHER INFORMATION: w can be a or t
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<222> LOCATION: (1)..(12)
<223> OTHER INFORMATION: y can be c or t
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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(12)
<223> OTHER INFORMATION: r can be a or g
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<223> OTHER INFORMATION: b can be c, g, or t

<400> SEQUENCE: 7

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cgcggtctgg cagtaaaaac tatccagcaa catttgggcc agctaaacat gcttcatcgt    300
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gatggcgatt ag                                                       1032
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What is claimed is:

1. A method for amplifying a target gene, said method comprising:
- contacting a transformant with a site-specific recombinase, wherein said transformant comprises a double-stranded DNA represented by a-b-c-d or a-c-b-d, wherein
  - one of a and b is a double-stranded DNA fragment comprising a first target sequence of a site-specific recombinase, and the other is a double-stranded DNA fragment comprising an inverted sequence of said first target sequence, wherein a first site specific recombination between a and b is induced by the site-specific recombinase; and
  - one of c and d is a double-stranded DNA fragment comprising a second target sequence of the site-specific recombinase and the other is a double-stranded DNA fragment comprising an inverted sequence of said second target sequence, wherein a second site specific recombination between c and d is induced by the site-specific recombinase;

and wherein
- a replication origin and at least one target gene to be amplified are inserted anywhere between a and d;
- arbitrary DNA sequences may be inserted among said fragments; and
- the first target sequence and the second target sequence of the site-specific recombinase are different; and
- the target gene is amplified by Double Rolling-Circle Replication (DRCR) comprising the first site specific recombination and the second site specific recombination.

2. The method of claim 1, wherein contacting the transformant with the site-specific recombinase includes any of the following steps:
- (1) introducing a plasmid constructed to express said site-specific recombinase;
- (2) transforming said transformant further to express said site-specific recombinase;
- (3) introducing directly said site-specific recombinase protein.

3. The method of claim 1, wherein b and c are combined and said double-stranded DNA is represented by a-b-d, wherein a and d are the same sequence with the same direction and the other letters are the same as defined previously.

4. The method of claim 1, wherein the double-stranded DNA is represented by a-b-X-c-d or a-c-X-b-d, wherein X represents a replication origin and the other letters are the same as defined previously.

5. The method of claim 4, wherein the double-stranded DNA is represented by a-A-b-X-c-B-d or a-A-c-X-b-B-d, wherein at least one of A and B represents the target gene, arbitrary DNA sequences may be inserted among these fragments, and the other letters are the same as defined previously.

6. The method of claim 1, wherein each of said the first and the second target sequences is selected from the group comprising loxP, lox511, lox5171, lox2272, lox2372, loxm2, loxFAS, lox71, lox66 and the mutants thereof in a case where the site-specific recombinase is Cre recombinase or its derivative; each of said the first and the second target sequences is selected from the group comprising FRT, F3, F5, FRT mutant−10, FRT mutant+10 and the mutants thereof in a case where the site-specific recombinase is Flp recombinase or its derivative; and each of said the first and the second target sequences is selected from the group comprising attB, attP and the mutants thereof in a case where the site-specific recombinase is phiC31 integrase or its derivative.

7. The method of claim 1, wherein the host is an animal cell.

8. A method for amplifying a target gene, said method comprising:
- (a) providing a double-stranded DNA represented by a-b-c-d or a-c-b-d, wherein
  - one of a and b is a double-stranded DNA fragment comprising a first target sequence of a site-specific recombinase, and the other is a double-stranded DNA fragment comprising an inverted sequence of said first target sequence, wherein a first site specific

recombination between a and b is induced by the site-specific recombinase; and

one of c and d is a double-stranded DNA fragment comprising a second target sequence of the site-specific recombinase and the other is a double-stranded DNA fragment comprising an inverted sequence of said second target sequence, wherein a second site specific recombination between c and d is induced by the site-specific recombinase;

and wherein

a replication origin and at least one target gene to be amplified are inserted anywhere between a and d;

arbitrary DNA sequences may be inserted among said fragments; and

the first target sequence and the second target sequence of the site-specific recombinase are different;

(b) obtaining a set of double-stranded DNA fragments by dividing the double stranded DNA of (a) into at least two, wherein

each said fragment contains a double-stranded DNA region with at least 50 bp at both ends for homologous recombination;

said double-stranded DNA region for homologous recombination comprises a part of the sequences of a host chromosome or an extrachromosomal element so that the double-stranded DNA can be integrated into the host chromosome or the extrachromosomal element by homologous recombination; and

said replication origin may be a replication origin of a host or an exogeneous origin;

(c) preparing a transformant, wherein said transformant is prepared by introducing into a host two kinds of the double-stranded DNA of (b), wherein said replication origin locates on a host chromosome or an extrachromosome; and

(d) affecting said transformant with the site-specific recombinase,

wherein the target gene is amplified by Double Rolling-Circle Replication (DRCR) comprising the first site specific recombination and the second site specific recombination.

9. The method of claim **8**, wherein the set of double-stranded DNA fragments comprises a double-stranded DNA fragment represented by e-a-A-b-f and a double-stranded DNA fragment represented by g-c-B-d-h, wherein one of a and b is a double-stranded DNA fragment comprising a first target sequence of a site-specific recombinase, and the other is a double-stranded DNA fragment comprising an inverted sequence of said first target sequence; and one of c and d is a double-stranded DNA fragment comprising a second target sequence of the site-specific recombinase and the other is a double-stranded DNA fragment comprising an inverted sequence of said second target sequence; each of letters from e to h is a double-stranded DNA fragment of at least 50 bp in size, which are arranged on a chromosome or an extra-chromosomal element that is a host for integration of the set of double-stranded DNA in order of e, f, a replication origin of the chromosome element or the extrachromosomal element, g and h; at least one of A and B represents the target gene to be amplified; and said replication origin or a part of it may be included in f or g; and an arbitrary DNA sequence may be inserted among these.

10. The method of claim **8**, wherein each of said the first and the second target sequences is selected from the group comprising loxP, lox511, lox5171, lox2272, lox2372, loxm2, loxFAS, lox71, lox66 and the mutants thereof in a case where the site-specific recombinase is Cre recombinase or its derivative; each of said the first and the second target sequences is selected from the group comprising FRT, F3, F5, FRT mutant−10, FRT mutant+10 and the mutants thereof in a case where the site-specific recombinase is Flp recombinase or its derivative; and each of said the first and the second target sequences is selected from the group comprising attB, attP and the mutants thereof in a case where the site-specific recombinase is phiC31 integrase or its derivative.

11. The method of claim **8**, wherein the host is an animal cell.

12. The method of claim **8**, wherein affecting the transformant with the site-specific recombinase includes any of the following steps:

(1) introducing a plasmid constructed to express said site-specific recombinase;

(2) transforming said transformant further to express said site-specific recombinase; and

(3) introducing directly said site-specific recombinase protein.

13. The method of claim **1**, wherein the double-stranded DNA is configured to generate in the host, after contacting the transformant with the site-specific recombinase, an amplification product comprising concatenated repeats of the double-stranded DNA between a and d, wherein regions between a and b, and/or between c and d, in the concatenated repeats may or may not be inverted in the amplification product relative to the orientation of corresponding regions in the double-stranded DNA.

14. The method of claim **1**, wherein the at least one target gene is amplified during a single cell cycle.

15. The method of claim **1**, wherein the replication origin is the replication origin of a host chromosome, fragments of a host chromosome, or an artificial chromosome.

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